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10. (Amended) A method according to claim 8 wherein said molecule introduces a restriction site in a region corresponding to an activator protein-3 motif (AP-3) and/or a basic transcription element (BTE).

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13. (Amended) A method according to claim 11 wherein said oligonucleotide molecule comprises the sequence designated 3A5R1 illustrated in Figure 6.

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16. (Amended) A method according to claim 14 wherein said molecule comprises the sequence designated 3A5F2 illustrated in Figure 6.

A7

19. (Amended) A molecule according to claim 17 which is capable of hybridising to an activator protein-3 motif (AP-3) or a basic transcription element.

20. (Amended) A molecule according to claim 17 which is capable of hybridising to a region comprising a polymorphic variant at at least one of positions -475 or -147 of the transcription regulatory region of the sequence encoding CYP3A5 illustrated in Figure 7.

21. (Amended) A molecule according to any of claim 17 which comprises any of the sequences designated 3A5F1, 3A5F2 or 3A5R1 illustrated in Figure 6.

22. (Amended) A kit for performing the method of claim 1 comprising an oligonucleotide molecule of at least 10 contiguous nucleotides capable of amplifying a DNA sequence to detect a wild type or polymorphic variant in a transcription regulatory region of a sequence encoding cytochrome CYP3A5 said associated with a high or low drug metabolising phenotype

A7 cont

respectively, which molecule is capable of hybridising to a region incorporating either a polymorphic variant or wild type nucleotide in said region, such that amplification of said wild type and polymorphic variants will proceed from said molecule only when an oligonucleotide includes a sequence corresponding to either said wild type or polymorphic variant characteristic of a high drug metabolising phenotype and means for contacting said molecule and said transcription regulatory region of the sequence encoding CYP3A5.

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28. (Amended) A method according to claim 26 comprising screening for said variant in an activator protein-3 motif (AP-3) and/or a basic transcription element (BTE) of said transcription regulatory region.

29. (Amended) A method according to claim 26, comprising screening for said variant at at least one of position -475 or -147 of the transcription regulatory region of the sequence encoding CYP3A5 the sequence of which region is illustrated in Figure 7.

30. (Amended) A method according to claim 26 comprising screening for both variants at position -475 or -147.

31. (Amended) A method according to claim 26 comprising screening for the presence or absence of variants $T_{-475}G$ and $A_{-147}G$ in said transcriptional regulatory control region.

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36. (Amended) A method according to claim 32 wherein said transcription regulatory region includes a mutation in a recognition site for a transcription factor of said regulatory region.